

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT
T-1 EXAMINATION, Sep 2018
B. Tech. (Bioinformatics) V Semester

COURSE CODE : 15B11BI511
COURSE NAME: Structural Bioinformatics

MAX MARKS : 15
MAX. TIME: 1 Hr.

*Note: All questions are compulsory. Attempt all questions of a particular section at one place.
Answer each question to the point.*

1. Describe the PDB file format. What information does ATOM, HETATM and REMARK sections hold? (3 marks)
2. How do proteins fold to adopt a three dimensional structure from its primary structure. Discuss briefly the energetics of protein folding. (3 marks)
3. What are protein domains? Why is it important to identify the domains to study proteins? What difficulties might you encounter in assigning domains to a polypeptide chain? (3 marks)
4. Why do we need a system of classification to study the proteins? What are the important classification systems based on the three dimensional structure of proteins? Why may different classification systems not agree with each other for all proteins? (3 marks)
5. Describe the hierarchical levels in CATH and SCOP. Contrast CATH classification with SCOP classification system. (3 marks)